RECEIVED

OCT 0 8 2004

PTO/SB/21 (04-04)
Approved for use through 07/31/2006. OMB 0651-0031
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

Application Number	09/990,080
Filing Date	November 21, 2001
First Named Inventor	Gregg B. Morin
Art Unit	1652
Examiner Name	Margorzata A. Walicka
Attorney Docket Number	018/258C

Total Number of Pages in This Submission: 32

ENCLOSURES *(Check all that apply)*

- ☐ Fee Transmittal Form (in duplicate)
  - ☐ Fee Attached
- ☐ Amendment/Reply (18 pages)
  - ☐ After Final
  - ☐ Affidavits/declaration(s)
- ☐ Extension of Time Request
- ☐ Express Abandonment Request
- ☐ Information Disclosure Statement
- ☐ Certified Copy of Priority Document(s)
- ☐ Response to Missing Parts/ Incomplete Application
  - ☐ Response to Missing Parts under 37 CFR 1.52 or 1.53
- ☐ Drawing(s)
- ☐ Licensing-related Papers
- ☐ Petition
- ☐ Petition to Convert to a Provisional Application
- ☐ Power of Attorney, Revocation Change of Correspondence Address
- ☐ Terminal Disclaimer
- ☐ Request for Refund
- ☐ CD, Number of CD(s) _____
- ☐ After Allowance communication to Technology Center (TC)
- ☐ Appeal Communication to Board of Appeals and Interferences
- ☐ Appeal Communication to TC (Appeal Notice, Brief, Reply Brief)
- ☐ Proprietary Information
- ☐ Status Letter
- ☑ Other Enclosure(s) (please identify below):

Remarks

Substitute Specification & Sequence Listing (30 pages)
Last page marker

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm or Individual name	J. Michael Schiff, Registration No. 40,253
Signature	
Date	Oct 8/04

CERTIFICATE OF TRANSMISSION/MAILING

I hereby certify that this correspondence is being facsimile transmitted to the USPTO or deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on the date shown below.

Typed or printed name	Sherry L. Murphy		
Signature		Date	10/8/04

This collection of information is required by 37 CFR 1.5. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to 2 hours to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

BEST AVAILABLE COPY

INACTIVE VARIANTS OF THE HUMAN TELOMERASE CATALYTIC SUBUNIT

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. patent application Ser. No. 09/128,354, filed Aug. 3, 1998, now U.S. Patent No. 6,337,200; which is a continuation-in-part of U.S. patent application Ser. No. 09/052,864, filed Mar. 31, 1998, now abandoned.

The aforelisted priority applications are hereby incorporated herein by reference in their entirety, as are the following: U.S. patent application Ser. Nos. 08/851,843; 08/854,050; 08/911,312; 08/912,951; 08/916,503; 08/974,549; and 08/974,584; and International Patent Publications WO 98/14592 and WO 98/14593.

FIELD

The present invention is related to the catalytic protein subunit of human telomerase. The invention provides methods and compositions relating to medicine, molecular biology, chemistry, pharmacology, and medical diagnostic and prognostic technology.

BACKGROUND

The following discussion is intended to introduce the field of the present invention to the reader. The citation of various references in this section should not be construed as an admission of prior invention.

It has long been recognized that complete replication of the ends of eukaryotic chromosomes requires specialized cell components (Watson, 1972, *Nature New Biol.*, 239:197; Olovnikov, 1973, *J. Theor. Biol.*, 41:181). Replication of a linear DNA strand by conventional DNA polymerase requires an RNA primer, and can proceed only 5' to 3'. When the RNA bound at the extreme 5' ends of eukaryotic chromosomal DNA strands is removed, a gap is introduced, leading to a progressive shortening of daughter strands with each round of replication. This shortening of telomeres, the protein-DNA structures physically located on the ends of chromosomes, is thought to account for the phenomenon of cellular senescence or aging of normal human somatic cells *in vitro* and *in vivo*. The maintenance of telomeres is a function of a telomere-specific DNA polymerase known as telomerase. Telomerase is a ribonucleoprotein (RNP) that uses a portion of its RNA moiety as a template for telomeric DNA synthesis (Morin, 1997, *Eur. J. Cancer* 33:750). The length and integrity of telomeres and the telomerase expression status of a cell is thus related to entry of a cell into a senescent stage (*i.e.*, loss of proliferative capacity), or the ability of a cell to escape senescence, *i.e.*, to become immortal.

Consistent with the relationship of telomeres and telomerase to the proliferative capacity of a cell (*i.e.*, the ability of the cell to divide indefinitely), telomerase activity is detected in immortal cell lines and an extraordinarily diverse set of tumor tissues, but is not detected (i.e., was absent or below the assay threshold) in normal somatic cell cultures or normal tissues adjacent to a tumor (see, U.S. Patent Nos. 5,629,154; 5,489,508; 5,648,215; and 5,639,613; see also, Morin, 1989, *Cell* 59: 521; Shay and Bacchetti 1997, *Eur. J. Cancer* 33:787; Kim et al., 1994, *Science* 266:2011; Counter et al., 1992, *EMBO J.* 11:1921; Counter et al., 1994, *Proc. Natl. Acad. Sci. U.S.A.* 91,

2900; Counter et al., 1994, *J. Virol.* 68:3410). Moreover, a correlation between the level of telomerase activity in a tumor and the likely clinical outcome of the patient has been reported (e.g., U.S. Patent No. 5,639,613, *supra*; Langford et al., 1997, *Hum. Pathol.* 28:416). Thus, human telomerase is an ideal target for diagnosing and treating human diseases relating to cellular proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell.

SUMMARY

In one aspect, the invention provides an isolated or recombinant hTRT polypeptide that has telomerase catalytic activity. In one embodiment, the hTRT polypeptide has a deletion of at least 25 residues in the regions corresponding to residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of hTRT. In a related embodiment, residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of hTRT are deleted. The invention also provides a polynucleotide comprising a nucleotide sequence encoding these hTRT polypeptides. In some embodiments, the polynucleotide includes a promoter sequence operably linked to the nucleotide sequence encoding the hTRT polypeptide.

The invention also provides a method of preparing recombinant telomerase by contacting a recombinant hTRT polypeptide containing a deletion as described *supra* with a telomerase RNA component under conditions such that the recombinant protein and the telomerase RNA component associate to form a telomerase enzyme capable of catalyzing the addition of nucleotides to a telomerase substrate. The hTRT polypeptide may be produced in an *in vitro* expression system and/or may be purified before the contacting step. In some embodiments, the contacting occurs in a cell.

The invention further provides a method for increasing the proliferative capacity of a vertebrate cell by introducing into a cell the recombinant hTRT polynucleotide encoding an hTRT deletion variant described *supra*. In a related embodiment, the invention provides a cell, such as a human cell or other mammalian cell, comprising a nucleotide sequence that encodes the hTRT deletion variant polypeptide. The invention provides such cells that have an increased proliferative capacity relative to a cell that is otherwise identical but does not comprise the recombinant polynucleotide.

In a different aspect of the invention, an isolated or recombinant hTRT polypeptide that has a deletion of amino acid residues 192-450, 560-565, 637-660, 638-660, 748-766, 748-764, or 1055-1071, where the residue numbering is with reference to the hTRT polypeptide having the sequence provided in FIG. 1, is provided. In one embodiment, the hTRT protein fragment has at least 6 amino acid residues. In other embodiments, the hTRT protein fragment has at least 8, at least about 10, at least about 12, at least about 15 or at least about 20 contiguous amino acid residues of a naturally occurring hTRT polypeptide. In still other embodiments, the hTRT protein fragment has at least about 50 or at least about 100 amino acid residues. In a related aspect, the invention provides an isolated, recombinant, or substantially purified polynucleotide encoding this polypeptide, which in some embodiments includes a promoter sequence operably linked to the nucleotide sequence encoding the hTRT polypeptide.

The invention also provides a method of reducing telomerase activity in a cell by introducing the polynucleotide described *supra* (i.e., having a deletion of deletion of amino acid residues 192-450, 560-565, 637-660, 638-660, 748-766, 748-764, or 1055-1071) into a cell under conditions in which it is expressed.

In a related embodiment, the hTRT polypeptide has one or more mutations other than, or in addition to, a deletion of at least 25 residues in the regions corresponding to residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of hTRT.

In an other embodiment, the invention provides &&& METHOD

DRAWINGS

Figure 1 shows the amino acid sequence of a 1132-residue human telomerase reverse transcriptase (hTRT) protein (SEQ. ID NO:2).

Figure 2 shows the nucleotide sequence of a naturally occurring cDNA encoding the hTRT protein (SEQ. ID NO:1).

DETAILED DESCRIPTION

I. Introduction

Telomerase is a ribonucleoprotein complex (RNP) comprising an RNA component and a catalytic protein component. The catalytic protein component of human telomerase, hereinafter referred to as telomerase reverse transcriptase ("hTRT"), has been cloned, and protein, cDNA and genomic sequences determined. See, e.g., Nakamura et al., 1997, Science 277:955, and U.S. Patent Nos. 6,475,789 and 6,166,178. The sequence of a full-length native hTRT has been deposited in GenBank (Accession No. AF015950), and plasmid and phage vectors having hTRT coding sequences have been deposited with the American Type Culture Collection, Rockville, Md. (accession numbers 209024, 209016, and 98505). The catalytic subunit protein of human telomerase has also been referred to as "hEST2" (Meyerson et al., 1997, Cell 90:785), "hTCS1" (Kilian et al., 1997, Hum. Mol. Genet. 6:2011), "TP2" (Harrington et al., 1997, Genes Dev. 11:3109), and "hTERT" (e.g., Greider, 1998, Curr. Biol 8:R178-R181). Human TRT is also described in the aforereferenced priority applications and U.S. patent application Ser. Nos. 08/846,017, 08/844,419, and 08/724,643. The RNA component of human telomerase (hTR) has also been characterized (see U.S. Pat. No. 5,583,016). All of the aforementioned applications and publications are incorporated by reference herein in their entirety and for all purposes.

Human TRT is of extraordinary interest and value because, inter alia, telomerase activity in human cells and other mammalian cells correlates with cell proliferative capacity, cell immortality, and the development of a neoplastic phenotype. Thus, hTRT polypeptides, including the hTRT variants described herein, and polynucleotides encoding hTRT polypeptides, are used, inter alia for conferring a telomerase activity (e.g., telomerase catalytic activity, infra) in a telomerase-negative cell such as a cell from a human, a mammal, a vertebrate, or other eukaryote (see, e.g., Bodnar et al., 1998, Science 279:349 and U.S. Patent Nos. 6,475,789 and 6,166,178). Variants that lack at least one hTRT activity (e.g., telomerase catalytic activity) are used, inter alia, to inhibit telomerase activity in a cell (e.g., by acting as "dominant negative mutants"). The hTRT variants and

polynucleotides encoding them, as described herein, are similarly useful in screening assays for identifying agents that modulate telomerase activity.

The hTRT variants of the present invention are characterized by one or more deletions or mutations, relative to a naturally occurring hTRT polypeptide, in defined regions of the protein, as `

Processive telomerase catalytic activity can be assayed by a variety of methods, including the "conventional assay" (Morin, 1989, *Cell* 59:521), the TRAP assay (U.S. Patent No. 5,629,154; see also, PCT publication WO 97/15687, PCT publication WO 95/13381; Krupp et al. *Nucleic Acids Res.*, 1997, 25: 919; Wright et al., 1995, *Nucl. Acids Res.* 23:3794), the "dot blot immunoassay" (U.S. Patent Application Serial Number 08/833,377), and other assays (e.g., Tatematsu et al., 1998, *Oncogene* 13:2265). The TRAPeze™ Kit (Oncor, Inc., Gaithersburg, MD) may be used. The telomerase substrate used in these assays may have a natural telomere sequence, or may be have a synthetic oligonucleotide with a different sequence (see, e.g., Morin, 1989, *Cell* 59:521; Morin, 1991, *Nature* 353:454-56).

As used herein, an hTRT variant is considered to have a specified activity if the activity is exhibited by either the hTRT variant polypeptide without an associated hTR RNA or in an hTRT-hTR complex. Each of the hTRT activities described supra is also described in detail in U.S. Patent Nos. 6,475,789 and 6,166,178.

II. hTRT Variants Described

a) hTRT Variants with Telomerase Catalytic Activity

It has now been demonstrated that large regions of the hTRT protein can be mutated (e.g., deleted) without loss of telomerase catalytic activity. Sites of mutation (e.g., deletion) are described herein with reference to the amino acid sequence provided in Figure 1 and encoded in plasmid pGRN121 (ATCC accession number 209016); however it will be recognized that the same or equivalent mutations may be made in other hTRT polypeptides, e.g., naturally occurring variants such as polymorphic variants, hTRT fusion proteins, hTRT homologs (e.g., from non-human species), and the like. For ease of discussion, the residues of the full-length hTRT protein having a sequence as provided in Figure 1 are referred to herein by number, with the amino-terminal methionine (M) in Figure 1 numbered "1", and the carboxy-terminal aspartic acid (D) numbered "1132".

Regions of the hTRT protein that can be mutated (e.g., deleted) without abolishing telomerase catalytic activity include the regions from amino acid residues 192 to 323 (inclusive) and residues 415 to 450 (inclusive). As is demonstrated in the experiments described *infra*, all or part of either of these regions, or all or part of both of them, can be deleted without abolishing the telomerase catalytic activity of the protein. The regions from amino acid residues 192 to 323 and residues 415 to 450 may be referred to as "nonessential" regions of hTRT (i.e., not essential for telomerase catalytic activity). Thus, in various embodiments, the hTRT variants of the invention comprise deletions of, or other mutations in, these nonessential regions of hTRT. As described in Section IV, *infra*, certain mutations (e.g., deletion of residues 415-450) alter RNA-binding characteristics of the hTRT variant.

Examples of mutations that can be made in the hTRT polypeptides of the invention include deletions, insertions, substitutions, and combination of mutations. Thus, in some embodiments the mutation is a deletion of at least one, typically at least about 10, and often at least about 25, at least about 50, or at least about 100 amino acid residues relative to a naturally occurring hTRT. In alternative embodiments, the mutation is a single amino acid substitution in a "non-essential" region, or a combinations of substitutions. Substitutions may be conservative substitutions or non-conservative substitutions. In still other embodiments, the mutation is an insertion or

substitution of amino acids, for example the insertion of residues that encode an epitope tag or novel proteolytic site. Substitutions may be of one or more (e.g., all) of the residues in the above-mentioned regions or may be combined with deletions so that, e.g., a shorter heterologous sequence is a substituted for a longer hTRT sequence. It will be appreciated, as noted *supra*, that in some embodiments the hTRT variant has more than one different type of mutation relative to a naturally occurring hTRT protein (e.g., a deletion and a point mutation).

The hTRT variants of the invention have certain advantages compared to naturally occurring hTRT proteins. In some embodiments, mutations may confer more efficient *in vitro* expression of active hTRT (e.g., in expression systems in which shorter polypeptides are more efficiently expressed than longer polypeptides), may provide sequences that aid in purification (e.g., an epitope tag sequence), or may add a new functional moiety to the hTRT polypeptide (e.g., a 3'→5' exonuclease domain from DNA polymerase I).

As noted supra, the hTRT variant polypeptides of the invention comprising mutations (e.g., deletions) in the "non-essential" regions of the hTRT retain telomerase catalytic activity. These variants, and polynucleotides that encode them, are useful in any application for which other catalytically active hTRT proteins (e.g., wild-type hTRT proteins) or polynucleotides may be used, including, inter alia, in therapeutic, diagnostic, and screening uses. Exemplary uses of hTRT polypeptides and polynucleotides are described in additional detail in the afore cited U.S. Patent Nos. 6,475,789 and 6,166,178.

In one embodiment, the hTRT variant of the invention is used to increase the proliferative capacity of a cell by, e.g., increasing telomerase activity in the cell (see, Bodnar et al. supra, and U.S. Patent Nos. 6,475,789 and 6,166,178 for a detailed description of exemplary methods). Briefly, in one embodiment, a polynucleotide comprising (i) a sequence encoding the hTRT variant polypeptide; (ii) an operably linked promoter (e.g., a heterologous promoter); and, (iii) optionally polyadenylation and termination signals, enhancers, or other regulatory elements, is introduced into a target cell (e.g., by transfection, lipofection, electroporation, or any other suitable method) under conditions in which the hTRT variant polypeptide is expressed. The expression in the cell of the catalytically active hTRT variant of the invention results in increased proliferative capacity (e.g., an immortal phenotype).

In another embodiment, the hTRT variant is used for in vitro reconstitution (IVR) of a telomerase ribonucleoprotein (e.g., comprising the hTRT variant polypeptide and a template RNA, e.g., hTR) that has telomerase catalytic activity. In vitro reconstitution methods are described in, e.g., Weinrich et al., 1997, Nat Genet. 17:498, and U.S. Patent Nos. 6,475,789 and 6,166,178. Briefly, in one embodiment, an expression vector encoding an hTRT variant of the invention is expressed in an in vitro expression system (e.g., a coupled transcription-translation reticulocyte lysate system such as that described in U.S. Pat. No. 5,324,637). In a particular embodiment, the hTRT variant polypeptide is coexpressed with hTR. In an alternative embodiment, the hTRT variant and hTR are separately expressed and then combined (mixed) in vitro. In the latter method, the hTR RNA and/or hTRT polypeptide may be purified before mixing. In this context, the hTRT polypeptide is "purified" when it is separated from at least one other component of the in vitro expression system, and it may be purified to homogeneity as determined by standard methods (e.g., SDS-PAGE). The in vitro reconstituted (IVR) telomerase has a variety of uses; in particular it is useful for identifying agents that modulate hTRT activity (e.g., drug screening assays).

(b) Deletion Variants Lacking Telomerase Catalytic Activity

In an other aspect, the invention provides hTRT deletion variants that lack telomerase catalytic activity (i.e., having less than 1% of the wild type activity), as well as polynucleotides encoding the variants lacking telomerase catalytic activity. In particular, the invention provides variants comprising one or more of the following deletions relative to wild-type hTRT: residues 192-450, 637-660, 638-660, 748-766, 748-764, and 1055-1071. These variants are referred to herein as "PCA$^-$ variants" (processive telomerase catalytic activity minus variants).

The PCA$^-$ variant proteins and polynucleotides of the invention lacking telomerase catalytic activity are used in, *inter alia*, therapeutic, screening and other applications. For example, PCA– variants are useful as dominant negative mutants for inhibition of telomerase activity in a cell. In one embodiment, a PCA$^-$ variant is introduced into a cell (e.g., by transfection with a polynucleotide expression vector expressing the PCA$^-$ variant), resulting in sequestration of a cell component (e.g., hTR) required for accurate telomere elongation. Thus, for example, administration of a polypeptide that binds hTR, a DNA primer, a telomerase-associated protein, or other cell component, but which does not have telomerase catalytic activity, is used to reduce endogenous telomerase activity in the cell or to otherwise interfere with telomere extension (e.g., by displacing active telomerase from telomeric DNA). Similarly, in certain embodiments, a PCA$^-$ variant of the invention having one or several hTRT activities (i.e., other than processive telomerase catalytic activity) is used for screening for agents that specifically modulate (inhibit or activate) a telomerase activity other than telomerase catalytic activity. The use of hTRT variants as dominant negative mutants, and in other applications, is described in detail in U.S. Patent Nos. 6,475,789 and 6,166,178.

III. Making hTRT Variants

The hTRT variant polypeptides and polynucleotides of the invention may be produced using any of a variety of techniques known in the art. In one embodiment, a polypeptide having the desired sequence, or a polynucleotide encoding the polypeptide, is chemically synthesized (see, e.g., Roberge, et al., 1995, *Science* 269:202; Brown et al., 1979, *Meth. Enzymol.* 68:109). More often, the hTRT variant polypeptides and polynucleotides of the invention are created by manipulation of a recombinant polynucleotide encoding an hTRT polypeptide. Examples of suitable recombinant polynucleotides include pGRN121, *supra*, and other hTRT cDNA and genomic sequences.

Methods for cloning and manipulation of hTRT encoding nucleic acids (e.g., site-specific mutagenesis, linker scanning mutagenesis, and the like) are well known in the art and are described, for example, in Sambrook et al., 1989, MOLECULAR CLONING: A LABORATORY MANUAL, 2ND ED., VOLS. 1-3, Cold Spring Harbor Laboratory, and Ausubel et al., 1997, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Greene Publishing and Wiley-Interscience, New York. One convenient method for producing a polynucleotide encoding a desired hTRT deletion variant is by restriction digestion and subsequent ligation of a hTRT polynucleotide, to remove a region(s) of the polynucleotide encoding the amino acid residues to be deleted. If desired, restriction sites can be introduced or removed from a synthetic or naturally occurring hTRT gene to facilitate the production and detection of variants.

Typically, the recombinant polynucleotide encoding an hTRT variant of the invention is linked to appropriate regulatory elements (e.g., promoters, enhancers, polyadenylation signals, and the like) and expressed in a cell free system (see, e.g., Weinrich et al., supra), in bacteria (e.g., E. coli), in ex vivo animal cell culture (see, e.g., Bodnar et al., supra), in animals or plants (e.g., transgenic organisms or in gene therapy applications), or by

any other suitable method. Suitable expression systems are well known in the art and include those described in Weinrich et al., and Bodnar et al., both supra, and in U.S. Patent Nos. 6,475,789 and 6,166,178.

Additional hTRT variants of the invention may be made using "DNA shuffling" *in vitro* recombination technology (see, e.g., Crameri et al., 1998, *Nature* 391:288-291; Patten et al., 1997, *Curr. Opin. Biotechnol.* 8:724-733, Stemmer, 1994, *Nature* 370:389-391; Crameri et al., 1996, *Nature Medicine,* 2:1-3; Crameri et al., 1996, *Nature Biotechnology* 14:315-319; WO 95/22625; Stemmer, 1995, *Science* 270:1510; Stemmer et al., *1995, Gene,* 164, 49-53; Stemmer, 1995, *Bio/Technology,* 13:549-553; Stemmer, 1994, *Proc. Natl. Acad. Sci. USA* 91:10747-10751). The specific deletion variants described *supra,* "wild-type hTRT" and non-human hTRT-homologs may be used in individually or various combinations as starting substrates to produce novel polypeptides with the desired activity. The activity or activities of the resulting polypeptides determined using the assays described in Section I, *supra.*

IV. Exemplary hTRT Variants

a) Generally

Exemplary hTRT variants were created by *in vitro* mutagenesis of polynucleotides encoding a full-length hTRT protein using the method of Perez et al., 1994, *J. Biol. Chem.* 269:22485-87. The mutant polynucleotides were expressed *in vitro* and telomerase reconstituted by *in vitro* mixing of hTRT and human telomerase RNA as described in Weinrich et al., 1997, *supra.* Reconstitution reactions were carried out using 0.5 pmole, 20 pmole, and, in some cases, other amounts of added hTR. Telomerase processive catalytic activity was assayed using a modified TRAP assay (Weinrich et al., 1997, *supra*). The results are summarized in Table 1.

TABLE 1

Deletion Name	Oligo	Amino acids deleted	Activity[1]
pGRN234	RT1 + RT2	none (delete *NcoI* site)	+
pGRN226	RT3A	192-323	+
RT3	RT3	200-326	+
pGRN237	RT4A	192-271	+
RT4	RT4	200-271	+
pGRN210	LM122-Nuc	222-240	+
pGRN235	RT5	415-450	+
pGRN242	RT3A+RT5	192-326 + 415-450	+
pGRN243	RT4A+RT5	192-271 + 415-450	+
pGRN240	RT3A/5	192-450	-
pGRN238	RT6A	637-660	-
RT6	RT 6	638-660	-
pGRN239	RT8A	748-766	-

TABLE 1

Deletion Name	Oligo	Amino acids deleted	Activity[1]
RT8	RT8	748-764	-
pGRN241	RT10	1055-1071	-
pGRN236	RT11	1084-1116	-
pGRN209	LM121-WG	930-934	-
pGRN231		560-565	-

"+" = at least 40% activity compared to *in vitro* reconsitution using wild-type hTRT (e.g., encoded by pGRN125; see Weinrich et al., 1997, *supra*)
"-" = less than 1% activity.

Certain of the hTRT variants described *supra* are altered in their ability to bind hTR. The variants encoded by pGRN235, pGRN242 and pGRN243 exhibited telomerase activity when 20 pmoles hTR (template RNA) was included in the reconstitution reaction, but showed a low or undetectable level of activity when 0.5 pmoles of hTR was used. The variable activity of these variants indicates that these variants have altered (e.g., decreased) hTR binding activity. Thus, the region from 415 to 450 is likely involved in RNA binding (e.g., by affecting the conformation of the protein).

This result suggests that the region immediately upstream of residue 415, corresponding to the conserved "CP" domain (Bryan et al., 1998, *Proc. Nat'l. Acad. Sci.* 95:8479-8484) is a region of contact between the hTRT protein and hTR (*e.g.*, corresponding to about residues 405 to 418 as set forth in Figure 1). This conclusion is supported by the relative lack of conservation of sequence when human and mouse TRT sequences are compared in the region corresponding to hTRT residues 415-450.

hTR binding to hTRT was also affected by mutations and deletions in the region 560-565. RNA binding was assayed by adding purified hTR to epitope tagged TRT proteins (*i.e.*, including a FLAG sequence; Immunex Corp, Seattle WA). The hTR and protein were incubated under conditions under which tagged "wild-type" hTRT associates with template RNA (hTR), and the hTRT protein or hTRT-hTR complex (if present) were immunoprecipitated. The precipitated complex was assayed for the presence and amount of associated RNA. Deletion of residues 560-565 dramatically decreased the binding of hTR by hTRT, with the concurrent expected decrease in telomerase activity (see Table 1, pGRN231). Mutation of phenylalanine (F) to alanine (A) mutation at position 561 of hTRT (the "F561A" variant; see, Weinrich et al., 1997, *supra*) resulted in reduced binding of hTR: this variant did not effectively bind hTR in association reactions when hTR was present at 0.5 pmoles, and showed less-than wild-type binding at 20 pmoles hTR. Mutation of tyrosine at 562 to alanine similarly resulted in a loss of hTR binding activity (e.g., about a 70-80% reduction compared to the wild-type sequence). Mutation of threonine at position 564 to alanine resulted in a decrease in RNA binding by approximately 20% compared to wild-type. In contrast, mutation of residues 560 (F) and 565 (E) to alanine did not affect hTR binding. These results indicate that the region from 560-565 is involved in RNA binding, e.g., by providing residues that contact hTR.

As will be apparent to one of skill advised of these results, the telomerase reconstitution may be inhibited using peptides comprising the sequence corresponding the hTRT residues 405-418, 560-565, or fragments thereof, or peptide mimetics of such sequences. Thus, in one embodiment of the present invention, telomerase

activity in a cell or an *in vitro* composition in which TRT protein and TR RNA are present, such as a telomerase reconstitution assay, is reduced by introducing to the cell or *in vitro* composition a polypeptide comprising the sequence FFYVTE (SEQ. ID NO:3), a polypeptide comprising the sequence YGVLLKTHCPLRAA (SEQ. ID NO:4), a polypeptide consisting essentially of FFYVTE (SEQ. ID NO:3), a polypeptide consisting essentially of FYVT (SEQ. ID NO:5), a polypeptide consisting essentially of YGVLLKTHCPLRAA (SEQ. ID NO:4), a fragment of at least three residues of the aforementioned polypeptides, or a peptide analog or mimetic of the polypeptide of any of the aforementioned compositions.

Peptide mimetics (or peptide analogs) are well known and are commonly used in the pharmaceutical industry as non-peptide drugs with properties analogous to those of the template polypeptide (Fauchere, 1986, *Adv. Drug Res.* 15:29; Veber et al., 1985, *TINS* p.392; and Evans et al., 1987, *J. Med. Chem.* 30:1229). Generally, peptidomimetics are structurally similar to the paradigm polypeptide having the sequence from hTRT but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of: $-CH_2NH-$, $-CH_2S-$, $-CH_2-CH_2-$, -CH'CH- (cis and trans), $-COCH_2-$, $-CH(OH)CH_2-$, and $-CH_2SO-$. Peptide mimetics may have significant advantages over polypeptide embodiments of this invention, including, for example: more economical production, greater chemical stability, enhanced pharmacological properties (half-life, absorption, potency, efficacy, etc.), altered specificity (e.g., a broad-spectrum of biological activities), reduced antigenicity, and others. In addition to modifications to the peptide backbone, synthetic or non-naturally occurring amino acids can also be used to substitute for the amino acids present in the polypeptide or in the functional moiety of fusion proteins. Synthetic or non-naturally occurring amino acids refer to amino acids which do not naturally occur in vivo but which, nevertheless, can be incorporated into the peptide structures described herein. Preferred synthetic amino acids are the d-α-amino acids of naturally occurring l-α-amino acid, mentioned above, as well as non-naturally occurring d- and l-α-amino acids represented by the formula H2NCHR5COOH where R5 is 1) a lower alkyl group, 2) a cycloalkyl group of from 3 to 7 carbon atoms, 3) a heterocycle of from 3 to 7 carbon atoms and 1 to 2 heteroatoms selected from the group consisting of oxygen, sulfur, and nitrogen, 4) an aromatic residue of from 6 to 10 carbon atoms optionally having from 1 to 3 substituents on the aromatic nucleus selected from the group consisting of hydroxyl, lower alkoxy, amino, and carboxyl, 5) -alkylene-Y where alkylene is an alkylene group of from 1 to 7 carbon atoms and Y is selected from the group consisting of (a) hydroxy, (b) amino, (c) cycloalkyl and cycloalkenyl of from 3 to 7 carbon atoms, (d) aryl of from 6 to 10 carbon atoms optionally having from 1 to 3 substituents on the aromatic nucleus selected from the group consisting of hydroxyl, lower alkoxy, amino and carboxyl, (e) heterocyclic of from 3 to 7 carbon atoms and 1 to 2 heteroatoms selected from the group consisting of oxygen, sulfur, and nitrogen, (f) -C(O)R2 where R2 is selected from the group consisting of hydrogen, hydroxy, lower alkyl, lower alkoxy, and -NR3R4 where R3 and R4 are independently selected from the group consisting of hydrogen and lower alkyl, (g) -S(O)nR6 where n is an integer from 1 to 2 and R6 is lower alkyl and with the proviso that R5 does not define a side chain of a naturally occurring amino acid. Other preferred synthetic amino acids include amino acids wherein the amino group is separated from the carboxyl group by more than one carbon atom such as β-alanine, γ-aminobutyric acid, and the like.

It will also be recognized by those of skill upon reviewing these results that the compositions (e.g., polypeptides and mimetics) described *supra* can be used to identify telomerase association and activity inhibitors other than the disclosed polypeptide and mimetics. These compositions may be used, for example, in rational drug design for *e.g.*, computer modeling of telomerase activity modulators (e.g., modulators that inhibit the association of TRT and TR or that catalyze the disassociation of the telomerase complex), as positive controls in

screens for modulators of telomerase activity, or in competition assays with candidate telomerase activity modulators.

b) Methods

Mutagenesis of the hTRT coding sequence of pGRN125 was carried out using the methods described by Perez et al., 1994, *J. Biol. Chem.* 269:22485-87. Most of the deletion mutants were generated from the plasmid pGRN125 (Weinrich et al., 1997, *supra*). Deletion mutants pGRN235 and pGRN236 were made in a secondary round of mutagenesis in an altered pGRN234. pGRN234 was generated by mutating (deleting) the *Nco* I site in pGRN125 (changing CAC to CAT in the histidine residue at position 754) and introducing a new *Nco*I site at the translation start site (ATG). Table 2 shows exemplary oligonucleotides used to generate the plasmids expressing the deletion variants of the invention.

TABLE 2

Oligo Name	Oligo sequence 5'-3'	length	Description	SEQ. ID NO:
RT1	GAAGGCCGCCCACGGGCACGTCC GC	25	Mutagenesis oligo to delete Nco I site from pGRN125	6
RT2	CCCGGCCACCCCAGCCATGGCGC GCGCTCCCC		Mutagenesis oligo to create Nco I site @ ATG of pGRN 125	7
RT5	TACGGGGTGCTCCTCAAGACGCAC TGCCCGCTGCTCCGCCAGCACAGC AGCCCCTGGCAG	60	Mutagenesis oligo to create a deletion of aa 415-450 in pGRN125	8
RT10	TACTCCATCCTGAAAGCCAAGAAC GCAGGGCTGTGCCACCAAGCATTC CTGCTCAAGCTG	60	Mutagenesis oligo to create a deletion of aa 1055-1071 in pGRN125	9
RT11	CTGTGCCACCAAGCATTCCTGCTC AAGCTGGCCGCAGCCAACCCGGC ACTGCCCTCAGAC	60	Mutagenesis oligo to create a deletion of aa 1083-1116 in pGRN125. Oligo creates a NheI site.	10
RT3A	ACTCAGGCCCGGCCCCCGCCACA CGCTAGCGAGACCAAGCACTTCCT CTACTCCTCAGGC	60	Mutagenesis oligo to create a deletion of aa 192-323 in pGRN125. Oligo creates a NheI site.	11
RT4A	ACTCAGGCCCGGCCCCCGCCACA CGCTAGCGTGGTGTCACCTGCCAG ACCCGCCGAAGAA	60	Mutagenesis oligo to create a deletion of aa 192-271 in pGRN125. Oligo creates a NheI site.	12
RT6A	ATCCCCAAGCCTGACGGGCTGCGG CCGATTGTTAACATGCTGTTCAGCG TGCTCAACTACGAGCGGGCG	69	Mutagenesis oligo to create a deletion of aa 638-660 in pGRN125. Oligo creates a Hpa I site.	13
RT8A	ACGTACTGCGTGCGTCGGTATGCC GTGGTCACAGATCTCCAGCCGTAC ATGCGACAGTTCGTG	63	Mutagenesis oligo to create a deletion of aa 748-766 in pGRN125. Oligo creates a Bgl II site.	14
RT3A/5	ACTCAGGCCCGGCCCCCGCCACA CGCTAGCCTGCTCCGCCAGCACAG CAGCCCCTGGCAG	60	Mutagenesis oligo to create a deletion of aa 192-450 in pGRN125. Oligo creates a NheI site.	15

TABLE 2

Oligo Name	Oligo sequence 5'-3'	length	Description	SEQ. ID NO:
LM121-WG	GTTCAGATGCCGGCCCACGGCCTA TTCCCTCTAGATACCCGGACCCTG GAGGTGCAGAGCGAC	63	Mutagenesis oligo to delete aa 930-934. Oligo introduces a new XbaI site	16
LM122-Nuc	CCCTGGGCCTGCCAGCCCCGGGT GCCGGCGCTGCCCCTGAGCCGGA GCGG	50	Mutagenesis oligo to delete aa 222-240. Oligo introduces a new Nae I site	17
RT3	GCTAGTGGACCCCGAAGGCGTCTG GGATGCGAGACCAAGCACTTCCTC TACTCCTCAGGC	60	Mutagenesis oligo to create a deletion of aa200-323 in pGRN125	18
RT4	GCTAGTGGACCCCGAAGGCGTCTG GGATGCGTGGTGTCACCTGCCAGA CCCGCCGAAGAA	60	Mutagenesis oligo to create a deletion of aa 200-271 in pGRN125	19
RT6	GACGGGCTGCGGCCGATTGTGAAC ATGGACCTGTTCAGCGTGCTCAAC TACGAGCGGGCG	60	Mutagenesis oligo to create a deletion of aa 638-660 in pGRN125	20
RT8	ACGTACTGCGTGCGTCGGTATGCC GTGGTCACCTTGACAGACCTCCAG CCGTACATGCGA	60	Mutagenesis oligo to create a deletion of aa 748-764 in pGRN125	21

V. Definitions

The following terms are defined *infra* to provide additional guidance to one of skill in the practice of the invention:

When comparing regions between a first and second polypeptide, sequences can be aligned by inspection (e.g., alignment of identical sequences) or by computer implemented alignment of the two sequences. Thus, for example, the residues 192 to 323 of the hTRT polypeptide having the sequence set forth in FIG. 1 "correspond" to residues in the same position in a hTRT polypeptide that differs from the FIG. 1 sequence due to polymorphic variation, or other mutations or deletions (e.g., when the two polypeptides are optimally aligned). Alignments may also be carried out using the GAP computer program, version 6.0 (Devereux et al, 1984, Nucl. Acid. Res. 12:387; available from the University of Wisconsin Genetics Computer Group, Madison, Wis.). The GAP program utilizes the alignment method of Needleham and Wunsch, 1970 J. Mol. Biol. 48: 443-453 as revised by Smith and Waterman, 1981, Adv. Appl. Math 2:482. The preferred default parameters for the GAP program include (1) the weighted comparison matrix of Gribskov and Burgess, 1986, Nucl. Acid. Res. 14:6745 as described by Schwartz and Dayhoff, eds., 1979, ATLAS OF PROTEIN SEQUENCE AND STRUCTURE, National Biomedical Research Foundation, pp. 353-358 (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps. Alternatively, alignments can be carried out using the BLAST algorithm, which is described in Altschul et al., 1990, J. Mol. Biol. 215:403-410 using as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915); alignments (B) of 50, expectation (E) of 10, M=5, and N=-4. A modification of BLAST, the "Gapped BLAST" allows

gaps to be introduced into the alignments that are returned (Altschul et al., 1997, Nucleic Acids Res 1:3389-3402). Software for performing BLAST analyses is publicly available through the Internet website of the National Center for Biotechnology Information.

As used herein, "stringent hybridization conditions" or "stringency" refers to conditions in a range from about 5°C. to about 20°C. or 25°C. below the melting temperature (T_m) of the target sequence and a probe with exact or nearly exact complementarity to the target. As used herein, the melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half-dissociated into single strands. Methods for calculating the T_m of nucleic acids are well known in the art (see, e.g., Berger and Kimmel (1987) METHODS IN ENZYMOLOGY, VOL. 152: GUIDE TO MOLECULAR CLONING TECHNIQUES, San Diego: Academic Press, Inc. and Sambrook et al. (1989) MOLECULAR CLONING: A LABORATORY MANUAL, 2ND ED., VOLS. 1-3, Cold Spring Harbor Laboratory hereinafter, "Sambrook"), both incorporated herein by reference). As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5+0.41(\%\ G+C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (see e.g., Anderson and Young, Quantitative Filter Hybridization in NUCLEIC ACID HYBRIDIZATION (1985)). Other references include more sophisticated computations which take structural as well as sequence characteristics into account for the calculation of T_m. The melting temperature of a hybrid (and thus the conditions for stringent hybridization) is affected by various factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, and the like), and the concentration of salts and other components (e.g., the presence or absence of formamide, dextran sulfate, polyethylene glycol). The effects of these factors are well known and are discussed in standard references in the art, e.g., Sambrook, supra and Ausubel et al. supra. Typically, stringent hybridization conditions are salt concentrations less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion at pH 7.0 to 8.3, and temperatures at least about 30°C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C. for long probes (e.g., greater than 50 nucleotides). As noted, stringent conditions may also be achieved with the addition of destabilizing agents such as formamide, in which case lower temperatures may be employed.

As used herein, the term "substantial identity," "substantial sequence identity," or "substantial similarity" in the context of nucleic acids, refers to a measure of sequence similarity between two polynucleotides. Substantial sequence identity can be determined by hybridization under stringent conditions, by direct comparison, or other means. For example, two polynucleotides can be identified as having substantial sequence identity if they are capable of specifically hybridizing to each other under stringent hybridization conditions. Other degrees of sequence identity (e.g., less than "substantial") can be characterized by hybridization under different conditions of stringency. Alternatively, substantial sequence identity can be described as a percentage identity between two nucleotide (or polypeptide) sequences. Two sequences are considered substantially identical when they are at least about 60% identical, preferably at least about 70% identical, or at least about 80% identical, or at least about 90% identical, or at least about 95% or 98% to 100% identical. Percentage sequence (nucleotide or amino acid) identity is typically calculated by determining the optimal alignment between two sequences and comparing the two sequences. For example an exogenous transcript used for protein expression can be described as having a certain percentage of identity or similarity compared to a reference sequence (e.g., the corresponding endogenous sequence). Optimal alignment of sequences may be conducted using the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2: 482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48: 443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad.

Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by inspection. The best alignment (i.e., resulting in the highest percentage of identity) generated by the various methods is selected. Typically these algorithms compare the two sequences over a "comparison window" (usually at least 18 nucleotides in length) to identify and compare local regions of sequence similarity, thus allowing for small additions or deletions (i.e., gaps). Additions and deletions are typically 20 percent or less of the length of the sequence relative to the reference sequence, which does not comprise additions or deletions. It is sometimes desirable to describe sequence identity between two sequences in reference to a particular length or region (e.g., two sequences may be described as having at least 95% identity over a length of at least 500 basepairs). Usually the length will be at least about 50, 100, 200, 300, 400 or 500 basepairs, amino acids, or other residues. The percentage of sequence identity is calculated by comparing two optimally aligned sequences over the region of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, or U) occurs in both sequences to yield the number of matched positions, and determining the number (or percentage) of matched positions as compared to the total number of bases in the reference sequence or region of comparison.

When referring to an "activity" of an hTRT variant, a variant is considered to be active in an assay of it displays at least 40% of the activity characteristic of the hTRT polypeptide having the sequence set forth in Fig. 1 ("wild type"). A variant is considered to lack activity when it has less that 1% of the "wild type" activity. A variant with greater than 1% activity and less than 40% activity has "intermediate activity."

As used herein, "conservative substitution," refers to substitution of amino acids with other amino acids having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar). The following six groups each contain amino acids that are conservative substitutions for one another: 1) alanine (A), serine (S), threonine (T); 2) aspartic acid (D), glutamic acid (E); 3) asparagine (N), glutamine (Q); 4) arginine (R), lysine (K); 5) isoleucine (I), leucine (L), methionine (M), valine (V); and 6) phenylalanine (F), tyrosine (Y), tryptophan (W) (see also, Creighton, 1984, PROTEINS, W. H. Freeman and Company).

All publications and patent documents cited in this application are incorporated by reference in their entirety and for all purposes to the same extent as if each individual publication or patent document were so individually denoted.